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Timestamp: [year=2008; month=12; day=3; hr=15; min=26; sec=33; ms=357; ]

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Application No: 10565183 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-11-12 13:40:37.377  
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No. of SeqIDs Defined: 8  
Actual SeqID Count: 8

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<110> Vermeij, Paul

<120> Hybrid Toxins Comprising Shiga-Like Toxin Subunits Fused to Escherichia Coli Heat Labile Enterotoxin Subunits and Vaccines Thereof

<130> 2003.006 US

<140> 10565183

<141> 2008-11-12

<150> PCT/EP04/51522

<151> 2004-07-16

<150> EP 03077266.9

<151> 2003-07-21

<160> 8

<170> PatentIn version 3.3

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48

ttt tct tcg gta tcc tat tcc cag gag ttt acg ata gac ttt tcg act

Phe Ser Ser Val Ser Tyr Ser Gln Glu Phe Thr Ile Asp Phe Ser Thr

20 25 30

96

caa caa agt tat gta tct tcg tta aat agt ata cgg aca gtg ata tcg

Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser

35 40 45

144

acc cct ctt gaa cat ata tct cag gga gct aca tcg gta tcc gtt att

Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile

50 55 60

192

aat cat aca cca cca gga agt tat att tcc gta ggt ata cga ggg ctt

Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu

65 70 75 80

240

gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga

Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg

85 90 95

288

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tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
115 120 125	
att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
130 135 140	
gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
145 150 155 160	
tca tat ctg gcg tta atg gag ttc agt ggt aat aca atg acc aga gat	528
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
165 170 175	
gca tca aga gca gtt ctg cgt ttt gtc act gtc aca gca gaa gcc tta	576
Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu	
180 185 190	
cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act	624
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr	
195 200 205	
gct cct gtt tat acg atg acg ccg gaa gac gtg gac ctc act ctg aac	672
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn	
210 215 220	
tgg ggg aga atc agc aat gtg ctt ccg gag tat cgg gga gag gct ggt	720
Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly	
225 230 235 240	
gtc aga gtg ggg aga ata tcc ttt aat aat ata tca gcg ata ctt ggt	768
Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly	
245 250 255	
act gtg gcc gtt ata ctg aat tgt gga aat tca tca aga aca atc aca	816
Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr	
260 265 270	
ggt gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc	864
Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu	
275 280 285	
agg gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag	912
Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln	
290 295 300	
tca gag gtt gac ata tat aac aga att cgg gat gaa tta tga	954
Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu	
305 310 315	

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catttaagag cggcgaaaca tttcaggtcg aagtccccggg cagtcaacat atagactccc 1194  
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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser  
35 40 45  
  
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile  
50 55 60  
  
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu  
65 70 75 80  
  
Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg  
85 90 95  
  
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe  
100 105 110  
  
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr  
115 120 125  
  
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala  
130 135 140

Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser  
145 150 155 160

Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp  
165 170 175

Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu  
180 185 190

Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr  
195 200 205

Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn  
210 215 220

Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly  
225 230 235 240

Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly  
245 250 255

Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr  
260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu  
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aatagtatac	ggacagtgat	atcgaccctt	cttgaacata	tatctcaggg	agctacatcg	180	
gtatccgtta	ttaatcatac	accaccagga	agttatat	ccgtaggtat	acgagggctt	240	
gatgtttatc	aggagcgttt	tgaccatctt	cgtctgatta	ttgaacgaaa	taatttatat	300	
gtggctggat	ttgttaatac	gacaacaaat	actttctaca	gattttcaga	ttttgcacat	360	
atatcattgc	ccggtgtgac	aactat	ttcc	atgacaacgg	acagcagtta	taccactctg	420
caacgtgtcg	cagcgctgga	acgttccgga	atgcaa	atca	gtcgtcactc	actgggtttca	480
tcatatctgg	cgttaatgga	gttcagtgg	t	aatacaatga	ccagagatgc	atcaagagca	540
gttctgcgtt	ttgtcactgt	cacagcagaa	gccttacgg	t	caggcaaat	acagagagaa	600
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ctcactctga	actgggggag	aatcagcaat	gtgcttccg	ag	tatcgggg	agaggctggt	720
gtcagagtgg	ggagaatatac	ctttaataat	atatcagcga	tacttggtac	tgtggccgtt	780	
atactgaatt	gtggaaattc	atcaagaaca	atcacaggtg	atacttgtaa	tgaggagacc	840	
cagaatctga	gcacaatata	tctcagggaa	tatcaatcaa	aagttaagag	gcagatat	ttt	900
tcagactatc	agtcagaggt	tgacatatat	aacagaattc	gggatgaatt	atg	aat	956
						Met Asn	
						1	
aaa gta aaa	tgt tat gtt	tta ttt acg	gcg tta cta	tcc tct cta	tat	1004	
Lys Val Lys	Cys Tyr Val	Leu Phe Thr	Ala Leu Leu	Ser Ser Leu	Tyr		
5	10	15					
gca cac gga	gct ccc cag	act att aca	gaa cta tgt	tcg gaa tat	cgc	1052	
Ala His Gly	Ala Pro Gln	Thr Ile Thr	Glu Leu Cys	Ser Glu Tyr	Arg		
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aac aca caa	ata tat acg	ata aat gac	aag ata cta	tca tat acg	gaa	1100	
Asn Thr Gln	Ile Tyr Thr	Ile Asn Asp	Lys Ile Leu	Ser Tyr Thr	Glu		
35	40	45	50				
tcg atg gca	ggc aaa aga	gaa atg gtt	atc att aca	ttt aag agc	ggc	1148	
Ser Met Ala	Gly Lys Arg	Glu Met Val	Ile Ile Thr	Phe Lys Ser	Gly		
55	60	65					
gaa aca ttt	cag gtc gaa	gtc ccg ggc	agt caa cat	ata gac tcc	cag	1196	
Glu Thr Phe	Gln Val Glu	Val Pro Gly	Ser Gln His	Ile Asp Ser	Gln		
70	75	80					
aaa aaa gcc	att gaa agg	atg aag gac	aca tta aga	atc aca tat	ctg	1244	
Lys Lys Ala	Ile Glu Arg	Met Lys Asp	Thr Leu Arg	Ile Thr Tyr	Leu		
85	90	95					

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Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys Thr Pro

100105110

aat tca att gcg gca atc agt atg aaa aac tag1325

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115120

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<400> 4

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202530

Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr

354045

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys

505560

Ser Gly Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp

65707580

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr

859095

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys

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Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn

115120

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tcataattca tcccgaattc tggtatatat gtc	33